SEQUENCE LISTING

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Phe Gly Tyr Thr Gly Pro Gln Gly Glu Tyr Ile Val Ala Leu Glu Asp
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        Gly Asp Cys Arg Gln Glu Leu Val Phe Ile Gly Gln Gly Leu Asp Thr
                355             360             365

        gac gcg tta cag cgc gag ctc gac cac tgc ctg ctg agc gcc cag gaa    1152
        Asp Ala Leu Gln Arg Glu Leu Asp His Cys Leu Leu Ser Ala Gln Glu
            370             375             380

10
        atc gcc gcc ggc cca ctg gcc tgg caa gcg ctg cca ggg gcg acc gcc    1200
        Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala
        385             390             395             400

15
        ttt gac cga cag acc ctt gcc cgc ccc cca cac agc cca tgg cga ttg    1248
        Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu
                405             410             415

        ccc cca ttt gat ccg aga tag                                        1269
        Pro Pro Phe Asp Pro Arg
20              420
```

```
30      Met Thr Asp Gly Ala Gln Ala Ser Arg Leu Pro Val Thr Val Leu Ser
        1               5               10              15


        Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg
35                  20              25              30


        Asn Arg Glu Gly Leu Arg Val Ala Val Ile Val Asn Asp Met Ser Glu
                35              40              45
40

        Val Asn Ile Asp Ala Glu Glu Val Gln Arg Asp Val Ala Leu His Arg
            50              55              60

45
        Gly Arg Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
        65              70              75              80


50      Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Met Leu Ala Arg Gln Gln
                        85              90              95


        Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
55                  100             105             110


        Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asp Gly Phe Ser Leu
            115             120             125
60
```

```
        Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Gly Ser
            130                 135                 140

  5     Arg Phe Gln Glu Leu Leu Glu Ser Pro His Thr Val Asp Gln Asp Asp
            145                 150                 155                 160

 10     Ala Thr Pro Asp Ala Pro Lys Arg His Leu Ala Asp Leu Leu Ile Glu
                        165                 170                 175

        Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Leu Asp Leu Ile
                    180                 185                 190
 15

        Asp Ala Ala Gln Tyr Gln Ala Val Gln Ala Ile Leu Thr Gly Leu Asn
                195                 200                 205
 20

        Pro Thr Ala Arg Ile Met Pro Met Ala His Gly Asn Ile Pro Ser Ala
            210                 215                 220

 25     Ser Leu Leu Gly Thr His Leu Phe Asp Leu Pro Ser Leu Ala Ala Ser
        225                 230                 235                 240

 30     Pro Gly Trp Met Arg Lys Met Glu Ala Ala Asp Ala Pro Ala Ser Glu
                        245                 250                 255

        Ser Asp Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Glu Arg Ala Pro
                    260                 265                 270
 35

        Phe His Pro Gln Arg Leu Leu Asp Phe Leu Gln Gln Pro Trp Cys Asn
                275                 280                 285
 40

        Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
            290                 295                 300

 45     Leu Glu Thr Gly Leu Leu Val Gln Ser Gly Lys Arg Phe Gln Trp Asp
        305                 310                 315                 320

 50     Tyr Val Gly Arg Trp Trp Asn Phe Ile Glu Pro Ser Gln Trp Pro Arg
                        325                 330                 335

        Asp Glu Tyr Arg Leu Gln Gly Ile Arg Ala Lys Trp Asp Ser Val Val
                    340                 345                 350
 55

        Gly Asp Cys Arg Gln Glu Leu Val Phe Ile Gly Gln Gly Leu Asp Thr
                355                 360                 365
 60

        Asp Ala Leu Gln Arg Glu Leu Asp His Cys Leu Leu Ser Ala Gln Glu
            370                 375                 380
```

```
      Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala
      385             390             395             400


 5    Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu
                      405             410             415


      Pro Pro Phe Asp Pro Arg
10                    420


      <210>   6
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15    <212>   DNA
      <213>   Pseudomonas putida


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20    <221>   CDS
      <222>   (1)..(582)
      <223>   Gen der Kodierregion der alpha-Untereinheit


      <220>
25    <221>   CDS
      <222>   (624)..(1286)
      <223>   Gen der Kodierregion der beta-Untereinheit


      <220>
30    <221>   gene
      <222>   (1283)..(2371)
      <223>   Gen des Aktivatorproteins


      <400>   6
35    atg acg gca act tca acc cct ggt gag cgg gca cgc gca ttg ttt gca      48
      Met Thr Ala Thr Ser Thr Pro Gly Glu Arg Ala Arg Ala Leu Phe Ala
      1               5                   10                  15


      gtg ctc aag cgc aaa gac ctc atc ccc gag ggc tac atc gaa cag ctc      96
40    Val Leu Lys Arg Lys Asp Leu Ile Pro Glu Gly Tyr Ile Glu Gln Leu
                      20                  25                  30


      acc cag ctg atg gaa cac ggc tgg agc ccg gaa aac ggc gcg cgc atc     144
      Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg Ile
45              35                  40                  45


      gtc gcc aag gcc tgg gtc gat ccg cag ttt cgc gag ctg ctc ctc aag     192
      Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Glu Leu Leu Leu Lys
              50                  55                  60
50

      gac ggt acg gcc gcc tgc gcc cag ttc ggc ttc acc ggc cca caa ggc     240
      Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Phe Thr Gly Pro Gln Gly
      65                  70                  75                  80


55    gaa tac atc gtc gcc ctg gaa gac acc ccg cag ttg aaa aac gtg atc     288
      Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Gln Leu Lys Asn Val Ile
                          85                  90                  95


      gtc tgt agc ctg tgc tcc tgc acg aac tgg ccg gtg ctg ggc ctg cca     336
60    Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu Pro
                          100                 105                 110
```

```
    cct gag tgg tac aag ggc ttc gag ttc cgt gcg cgg ttg gtc cgg gag      384
    Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg Glu
            115             120             125

 5  ggg cgc acg gta ttg cgc gag ctg ggc acc gag ttg ccc ggc gac atg      432
    Gly Arg Thr Val Leu Arg Glu Leu Gly Thr Glu Leu Pro Gly Asp Met
            130             135             140

10  gtg gtc aag gtc tgg gac acc agc gct gaa agc cgc tac ctg gtg ctg      480
    Val Val Lys Val Trp Asp Thr Ser Ala Glu Ser Arg Tyr Leu Val Leu
    145             150             155             160

    ccg caa cga cca gcg ggc tca gag cat atg agc gaa gag cag ttg cgg      528
    Pro Gln Arg Pro Ala Gly Ser Glu His Met Ser Glu Glu Gln Leu Arg
15                  165             170             175

    caa ctg gtc acc aag gac gtg ctg atc ggc gtc gcc ctg ccc cgc gtt      576
    Gln Leu Val Thr Lys Asp Val Leu Ile Gly Val Ala Leu Pro Arg Val
                180             185             190
20
    ggc tga gcaaggccgc ccaaccccat tcaacttccg gagtgttcaa t atg gat ggc  632
    Gly                                                   Met Asp Gly
                                                              195

25  ttt cac gat ctc ggc ggt ttc cag ggc ttt ggc aaa gtg ccc cac cgc      680
    Phe His Asp Leu Gly Gly Phe Gln Gly Phe Gly Lys Val Pro His Arg
                200             205             210

    atc aac agc ctg agc tac aag cag gtg ttc aag cag gac tgg gaa cac      728
30  Ile Asn Ser Leu Ser Tyr Lys Gln Val Phe Lys Gln Asp Trp Glu His
                215             220             225

    ctg gcc tac agc ctg atg ttc atc ggc gtc gac cac ctg aac aag ttc      776
    Leu Ala Tyr Ser Leu Met Phe Ile Gly Val Asp His Leu Asn Lys Phe
35          230             235             240

    agc gtc gac gaa ata cgt cat gcc gtc gaa cgc att gac gtg cgc cag      824
    Ser Val Asp Glu Ile Arg His Ala Val Glu Arg Ile Asp Val Arg Gln
    245             250             255             260
40
    cac gtc ggc acc gaa tac tac gaa cgt tat gtg atc gcc act gcc acg      872
    His Val Gly Thr Glu Tyr Tyr Glu Arg Tyr Val Ile Ala Thr Ala Thr
                265             270             275

45  ctg ctg gtc gaa aca ggc gtc atc acc cag gcc gaa ctg gat gaa gca      920
    Leu Leu Val Glu Thr Gly Val Ile Thr Gln Ala Glu Leu Asp Glu Ala
                280             285             290

    ctc ggc tcg cac ttc aag ctg gcc aac ccc gcc cat gcg caa ggg cgt      968
50  Leu Gly Ser His Phe Lys Leu Ala Asn Pro Ala His Ala Gln Gly Arg
                295             300             305

    gct gca att atc ggg cga gcg cct ttt gaa gtg ggc gat cgg gtc atc     1016
    Ala Ala Ile Ile Gly Arg Ala Pro Phe Glu Val Gly Asp Arg Val Ile
55          310             315             320

    gta cgc gat gaa tac gtg gcc ggg cat gtg cgc atg cct gca tac gtg     1064
    Val Arg Asp Glu Tyr Val Ala Gly His Val Arg Met Pro Ala Tyr Val
    325             330             335             340
60
```

```
     cgc ggc aag caa ggc gta gtg ctg cac cgg acc act gaa cag tgg ccg      1112
     Arg Gly Lys Gln Gly Val Val Leu His Arg Thr Thr Glu Gln Trp Pro
                     345             350                 355

 5   ttt ccg gac gcg att ggc cat ggc gac cag agc gct gcg cat caa ccg      1160
     Phe Pro Asp Ala Ile Gly His Gly Asp Gln Ser Ala Ala His Gln Pro
                     360             365             370

10   acc tac cat gtc gag ttc cgc gtg cgg gac ctg tgg ggc gat gcc gca      1208
     Thr Tyr His Val Glu Phe Arg Val Arg Asp Leu Trp Gly Asp Ala Ala
                 375             380             385

     gac gac ggc ctg gtg gtg gta gac ctg ttc gaa agc tat ctg gac agg      1256
     Asp Asp Gly Leu Val Val Val Asp Leu Phe Glu Ser Tyr Leu Asp Arg
15       390             395             400

     gtc gaa agc ccg cga gtg gtg cgc gca tga gtgccggcgc ccaggcaggc        1306
     Val Glu Ser Pro Arg Val Val Arg Ala
     405             410
20
     cggctgccgg tgacggtcct ttcaggcttc ctcggcgcag gcaagaccac cctgctcaac    1366

     cacatcctgc gcaaccgcca gggcctgaag gtggcggtta tcgtcaatga catgagcgag    1426

25   gtcaacatcg atgccgccca ggtccagcgc gacgttgcgc tgtatcgtgg ccaggatgaa    1486

     ttgatagaga tgagcaacgg ctgtatctgc tgcaccctgc gcgccgacct gcttgagcag    1546

     atcagcgcgc tggcgcgcca gcagcgtttc gattacctgt tgatcgagtc caccgggatt    1606
30
     tccgagccga tgccagtcgc cgagaccttt gcctttctcg acgccaacgg tttcagcctc    1666

     agcgaactgg cgcggctgga tacgctggtg acggtggtcg atgccagcca gttcatggcc    1726

35   atgctcgact ctcccgaaac cgtcgcgcgg gccgacgtca ccacggatga cagcaggcgc    1786

     ccgctggccg atctgctgat cgagcaggtc gagtatgcca atgtgattct ggtcaacaaa    1846

     cgcgacctgg tcgacgaggc gcagtaccag gccctgcagg cagttctcgc cgggctcaat    1906
40
     ccaggcgcac agatcctgcc gatggtggcc ggcaacgtcg ccctgtcgag cgtccttggt    1966

     acccagctgt cgatttgcc cagccttgcc gcagcgcccg gctggatgaa acagatggac     2026

45   gcgcacgaca ccccggccgg cgagtcgcag acctatggcg tgacgtcatg ggtgtaccga     2086

     gcgcgcgccc cgttccatcc gcaacgcttg cttgattttc tcgcccggcc ctggcgcgac    2146

     ggccgtcttc tgcgcagcaa aggttatttc tggcttgcca gccgccaccg cgaaatcggc    2206
50
     ttgctggtac acagcggcca gcagtttcaa tgggactatg ttggccattg gtggaacttc    2266

     atcgacacgt cacagtggcc acaggacaag tatcgcttgc agggcatcat ggccaagtgg    2326

55   gacagcatcg tcggcgactg ccgacaggag ctgaaaagct tatga                    2371
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<212> PRT
<213> Pseudomonas putida

<400> 7

Met Thr Ala Thr Ser Thr Pro Gly Glu Arg Ala Arg Ala Leu Phe Ala
1   5   10   15

Val Leu Lys Arg Lys Asp Leu Ile Pro Glu Gly Tyr Ile Glu Gln Leu
            20   25   30

Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg Ile
        35   40   45

Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Glu Leu Leu Leu Lys
    50   55   60

Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Phe Thr Gly Pro Gln Gly
65   70   75   80

Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Gln Leu Lys Asn Val Ile
            85   90   95

Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu Pro
            100   105   110

Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg Glu
        115   120   125

Gly Arg Thr Val Leu Arg Glu Leu Gly Thr Glu Leu Pro Gly Asp Met
    130   135   140

Val Val Lys Val Trp Asp Thr Ser Ala Glu Ser Arg Tyr Leu Val Leu
145   150   155   160

Pro Gln Arg Pro Ala Gly Ser Glu His Met Ser Glu Glu Gln Leu Arg
            165   170   175

Gln Leu Val Thr Lys Asp Val Leu Ile Gly Val Ala Leu Pro Arg Val
            180   185   190

Gly

<210> 8
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<212> PRT
<213> Pseudomonas putida

<400> 8

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        Met Asp Gly Phe His Asp Leu Gly Gly Phe Gln Gly Phe Gly Lys Val
        1               5                   10                  15

        Pro His Arg Ile Asn Ser Leu Ser Tyr Lys Gln Val Phe Lys Gln Asp
                    20                  25                  30

        Trp Glu His Leu Ala Tyr Ser Leu Met Phe Ile Gly Val Asp His Leu
                35                  40                  45

        Asn Lys Phe Ser Val Asp Glu Ile Arg His Ala Val Glu Arg Ile Asp
            50                  55                  60

        Val Arg Gln His Val Gly Thr Glu Tyr Tyr Glu Arg Tyr Val Ile Ala
        65                  70                  75                  80

        Thr Ala Thr Leu Leu Val Glu Thr Gly Val Ile Thr Gln Ala Glu Leu
                    85                  90                  95

        Asp Glu Ala Leu Gly Ser His Phe Lys Leu Ala Asn Pro Ala His Ala
                    100                 105                 110

        Gln Gly Arg Ala Ala Ile Ile Gly Arg Ala Pro Phe Glu Val Gly Asp
                115                 120                 125

        Arg Val Ile Val Arg Asp Glu Tyr Val Ala Gly His Val Arg Met Pro
            130                 135                 140

        Ala Tyr Val Arg Gly Lys Gln Gly Val Val Leu His Arg Thr Thr Glu
        145                 150                 155                 160

        Gln Trp Pro Phe Pro Asp Ala Ile Gly His Gly Asp Gln Ser Ala Ala
                    165                 170                 175

        His Gln Pro Thr Tyr His Val Glu Phe Arg Val Arg Asp Leu Trp Gly
                    180                 185                 190

        Asp Ala Ala Asp Asp Gly Leu Val Val Val Asp Leu Phe Glu Ser Tyr
                195                 200                 205

        Leu Asp Arg Val Glu Ser Pro Arg Val Val Arg Ala
            210                 215                 220

        <210>   9
        <211>   1089
        <212>   DNA
        <213>   Pseudomonas putida
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<223>  Gen der Kodierregion des Aktivatorproteins

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atg agt gcc ggc gcc cag gca ggc cgg ctg ccg gtg acg gtc ctt tca      48
Met Ser Ala Gly Ala Gln Ala Gly Arg Leu Pro Val Thr Val Leu Ser
1               5                   10                  15

ggc ttc ctc ggc gca ggc aag acc acc ctg ctc aac cac atc ctg cgc      96
Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg
                20                  25                  30

aac cgc cag ggc ctg aag gtg gcg gtt atc gtc aat gac atg agc gag     144
Asn Arg Gln Gly Leu Lys Val Ala Val Ile Val Asn Asp Met Ser Glu
            35                  40                  45

gtc aac atc gat gcc gcc cag gtc cag cgc gac gtt gcg ctg tat cgt     192
Val Asn Ile Asp Ala Ala Gln Val Gln Arg Asp Val Ala Leu Tyr Arg
        50                  55                  60

ggc cag gat gaa ttg ata gag atg agc aac ggc tgt atc tgc tgc acc     240
Gly Gln Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
65                  70                  75                  80

ctg cgc gcc gac ctg ctt gag cag atc agc gcg ctg gcg cgc cag cag     288
Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Ala Leu Ala Arg Gln Gln
                85                  90                  95

cgt ttc gat tac ctg ttg atc gag tcc acc ggg att tcc gag ccg atg     336
Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
            100                 105                 110

cca gtc gcc gag acc ttt gcc ttt ctc gac gcc aac ggt ttc agc ctc     384
Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asn Gly Phe Ser Leu
        115                 120                 125

agc gaa ctg gcg cgg ctg gat acg ctg gtg acg gtg gtc gat gcc agc     432
Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Ala Ser
        130                 135                 140

cag ttc atg gcc atg ctc gac tct ccc gaa acc gtc gcg cgg gcc gac     480
Gln Phe Met Ala Met Leu Asp Ser Pro Glu Thr Val Ala Arg Ala Asp
145                 150                 155                 160

gtc acc acg gat gac agc agg cgc ccg ctg gcc gat ctg ctg atc gag     528
Val Thr Thr Asp Asp Ser Arg Arg Pro Leu Ala Asp Leu Leu Ile Glu
                165                 170                 175

cag gtc gag tat gcc aat gtg att ctg gtc aac aaa cgc gac ctg gtc     576
Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Arg Asp Leu Val
            180                 185                 190

gac gag gcg cag tac cag gcc ctg cag gca gtt ctc gcc ggg ctc aat     624
Asp Glu Ala Gln Tyr Gln Ala Leu Gln Ala Val Leu Ala Gly Leu Asn
            195                 200                 205

cca ggc gca cag atc ctg ccg atg gtg gcc ggc aac gtc gcc ctg tcg     672
Pro Gly Ala Gln Ile Leu Pro Met Val Ala Gly Asn Val Ala Leu Ser
        210                 215                 220
```

```
agc gtc ctt ggt acc cag ctg ttc gat ttg ccc agc ctt gcc gca gcg    720
Ser Val Leu Gly Thr Gln Leu Phe Asp Leu Pro Ser Leu Ala Ala Ala
225             230             235             240

ccc ggc tgg atg aaa cag atg gac gcg cac gac acc ccg gcc ggc gag    768
Pro Gly Trp Met Lys Gln Met Asp Ala His Asp Thr Pro Ala Gly Glu
                245             250             255

tcg cag acc tat ggc gtg acg tca tgg gtg tac cga gcg cgc gcc ccg    816
Ser Gln Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Ala Arg Ala Pro
                260             265             270

ttc cat ccg caa cgc ttg ctt gat ttt ctc gcc cgg ccc tgg cgc gac    864
Phe His Pro Gln Arg Leu Leu Asp Phe Leu Ala Arg Pro Trp Arg Asp
            275             280             285

ggc cgt ctt ctg cgc agc aaa ggt tat ttc tgg ctt gcc agc cgc cac    912
Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
        290             295             300

cgc gaa atc ggc ttg ctg gta cac agc ggc cag cag ttt caa tgg gac    960
Arg Glu Ile Gly Leu Leu Val His Ser Gly Gln Gln Phe Gln Trp Asp
305             310             315             320

tat gtt ggc cat tgg tgg aac ttc atc gac acg tca cag tgg cca cag   1008
Tyr Val Gly His Trp Trp Asn Phe Ile Asp Thr Ser Gln Trp Pro Gln
                325             330             335

gac aag tat cgc ttg cag ggc atc atg gcc aag tgg gac agc atc gtc   1056
Asp Lys Tyr Arg Leu Gln Gly Ile Met Ala Lys Trp Asp Ser Ile Val
                340             345             350

ggc gac tgc cga cag gag ctg aaa agc tta tga                       1089
Gly Asp Cys Arg Gln Glu Leu Lys Ser Leu
            355             360
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<211>    362
<212>    PRT
<213>    Pseudomonas putida

<400>    10

Met Ser Ala Gly Ala Gln Ala Gly Arg Leu Pro Val Thr Val Leu Ser
1               5               10              15


Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg
            20              25              30


Asn Arg Gln Gly Leu Lys Val Ala Val Ile Val Asn Asp Met Ser Glu
        35              40              45


Val Asn Ile Asp Ala Ala Gln Val Gln Arg Asp Val Ala Leu Tyr Arg
    50              55              60


Gly Gln Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
65              70              75              80
```

```
         Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Ala Leu Ala Arg Gln Gln
                         85                  90                  95

  5      Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
                     100                 105                 110

 10      Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asn Gly Phe Ser Leu
                     115                 120                 125

         Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Ala Ser
 15              130                 135                 140

         Gln Phe Met Ala Met Leu Asp Ser Pro Glu Thr Val Ala Arg Ala Asp
             145                 150                 155                 160
 20
         Val Thr Thr Asp Asp Ser Arg Arg Pro Leu Ala Asp Leu Leu Ile Glu
                         165                 170                 175

 25      Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Arg Asp Leu Val
                     180                 185                 190

         Asp Glu Ala Gln Tyr Gln Ala Leu Gln Ala Val Leu Ala Gly Leu Asn
 30              195                 200                 205

         Pro Gly Ala Gln Ile Leu Pro Met Val Ala Gly Asn Val Ala Leu Ser
             210                 215                 220
 35
         Ser Val Leu Gly Thr Gln Leu Phe Asp Leu Pro Ser Leu Ala Ala Ala
             225                 230                 235                 240
 40
         Pro Gly Trp Met Lys Gln Met Asp Ala His Asp Thr Pro Ala Gly Glu
                         245                 250                 255

 45      Ser Gln Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Ala Arg Ala Pro
                     260                 265                 270

         Phe His Pro Gln Arg Leu Leu Asp Phe Leu Ala Arg Pro Trp Arg Asp
 50              275                 280                 285

         Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
             290                 295                 300
 55
         Arg Glu Ile Gly Leu Leu Val His Ser Gly Gln Gln Phe Gln Trp Asp
             305                 310                 315                 320
 60
         Tyr Val Gly His Trp Trp Asn Phe Ile Asp Thr Ser Gln Trp Pro Gln
                         325                 330                 335
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```
            Asp Lys Tyr Arg Leu Gln Gly Ile Met Ala Lys Trp Asp Ser Ile Val
                    340                 345                 350


     5      Gly Asp Cys Arg Gln Glu Leu Lys Ser Leu
                    355                 360



            <210>  11
    10      <211>  30
            <212>  DNA
            <213>  Artificial Sequence

            <220>
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            <400>  11
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            <210>  12
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            <212>  DNA
            <213>  Artificial Sequence
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            <220>
            <223>  Primer 1R

            <400>  12
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            <210>  13
            <211>  25
    35      <212>  DNA
            <213>  Artificial Sequence

            <220>
            <223>  Primer 2F
    40
            <400>  13
            atgacggcaa cttcaacccc tggtg                                       25


    45      <210>  14
            <211>  20
            <212>  DNA
            <213>  Artificial Sequence

    50      <220>
            <223>  Primer 2R

            <400>  14
            tcagctcctg tcggcagtcg                                             20
    55
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